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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=12; day=14; hr=12; min=36; sec=5; ms=475; ]

## Validated By CRFValidator v 1.0.3

Application No: 08793408 Version No: 1.0

Input Set:

Output Set:

**Started:** 2010-12-14 11:55:31.972

Finished: 2010-12-14 11:55:32.885

**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 913 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 18

Actual SeqID Count: 18

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (ii) TITLE OF INVENTION: Improvements in or Relating to Binding Proteins for Recognition of DNA
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
  - (B) STREET: 1100 New York Avenue, N.W.
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3918
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: Word Perfect
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08793408
  - (B) FILING DATE: 1997-06-02
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/GB95/01949
  - (B) FILING DATE: 17-AUG-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9514698.1
  - (B) FILING DATE: 18-JUL-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9422534.9
  - (B) FILING DATE: 08-NOV-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9416880.4
  - (B) FILING DATE: 20-AUG-1994
- (2) INFORMATION FOR SEQ ID NO: 1:

(A) LENGTH: 60 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
TCCTGCAGT TGGACCTGTG CCATGGCCGG CTGGGCCGCA TAGAATGGAA	
AACTAAAGC	
2) INFORMATION FOR SEQ ID NO: 2:	
Z) INCORMITON COR DEQ ID NO. Z.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 92 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS:	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: protein	
(,,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
Met Ala Glu Glu Arg Pro Tyr Ala Cys Pro	
met ara gru gru arg pro ryr ara cys pro	
Val Glu Ser Cys Asp Arg Arg Phe Ser Arg	
15 20	
Ser Asp Glu Leu Thr Arg His Ile Arg Ile	
25 30	
His Thr Gly Gln Lys Pro Phe Gln Cys Arg	
35 40	
Ile Cys Met Arg Asn Phe Ser Xaa Xaa Xaa	
45 50	
Xaa Leu Xaa Xaa His Xaa Arg Thr His Thr	
55 60	
Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys	
65 70	
Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg	
75 80	
Iva Ara Uia The Iva Ilo Iiia Iou Ara Cla	
Lys Arg His Thr Lys Ile His Leu Arg Gln 85	
Lys Asp	
2) INFORMATION FOR SEQ ID NO: 3:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(i) SEQUENCE CHARACTERISTICS:

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		(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
TATO	GACTTO	GG ATGGGAGACC GCCTGG	26
(2)	INFO	RMATION FOR SEQ ID NO: 4:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 28 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
AATT	CCAG	GC GGTCTCCCAT CCAAGTCA	28
(2)	INFO	RMATION FOR SEQ ID NO: 5:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
TATA	ATAGCO	GT GGGCGTATAT A	21
(2)	INFO	RMATION FOR SEQ ID NO: 6:	
		SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
caci			0.4
GCG	ratat <i>a</i>	AC GCCCACGCTA TATA	24
(2)	INFO	RMATION FOR SEQ ID NO: 7:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
TATA	ATAGCO	GN NNGCGTATAT A	21

(B) TYPE: nucleic acid

(2) INFORMATION FOR SEQ ID NO: 8:

	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
GCG1	CATATA	AC GCNNNCGCTA TATA	24
(2)	INFO	RMATION FOR SEQ ID NO: 9:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TTCC	CATGG	AG ACGCAGAAGC CCTTCAGCGG CCA	33
(2)	INFO	RMATION FOR SEQ ID NO: 10:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
TTCC	CATGGZ	AG ACGCAGGTGA GTTCCTCACG CCA	33
(2)	INFO	RMATION FOR SEQ ID NO: 11:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
CCC	CTTTC	TC TTCCAGAAGC CCTTCAGCGG CCA	33
(2)	INFO	RMATION FOR SEQ ID NO: 12:	
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 33 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS:  (D) TOPOLOGY: unknown	

(ii) MOLECULE TYPE: peptide

Met Ala Glu Glu Lys Pro Phe Gln Cys Arg 5 10						
Ile Cys Met Arg Asn Phe Ser Asp Arg Ser 15 20						
Ser Leu Thr Arg His Thr Arg His Thr Gly 25 30						
Glu Lys Pro						
(2) INFORMATION FOR SEQ ID NO: 13:						
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 33 amino acids</li><li>(B) TYPE: amino acid</li><li>(C) STRANDEDNESS:</li><li>(D) TOPOLOGY: unknown</li></ul>						
(ii) MOLECULE TYPE: peptide						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:						
Met Ala Glu Glu Lys Pro Phe Gln Cys Arg 5 10						
Ile Cys Met Arg Asn Phe Ser Glu Arg Gly 15 20						
Thr Leu Ala Arg His Glu Lys His Thr Gly 25 30						
Glu Lys Pro						
(2) INFORMATION FOR SEQ ID NO: 14:						
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 27 amino acids</li><li>(B) TYPE: amino acid</li><li>(C) STRANDEDNESS:</li><li>(D) TOPOLOGY: linear</li></ul>						
(ii) MOLECULE TYPE: peptide						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:						
Phe Gln Cys Arg Ile Cys Met Arg Asn Phe 5 10						
Ser Gln Gly Gly Asn Leu Val Arg His Leu 15 20						
Arg His Thr Gly Glu Lys Pro 25						

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: Phe Gln Cys Arg Ile Cys Met Arg Asn Phe 10 Ser Gln Ala Gln Thr Leu Gln Arg His Leu 15 20 Lys His Thr Gly Glu Lys 25 (2) INFORMATION FOR SEQ ID NO: 16: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16: Phe Gln Cys Arg Ile Cys Met Arg Asn Phe 5 10 Ser Gln Ala Ala Thr Leu Gln Arg His Leu 15 20 Lys His Thr Gly Glu Lys 25 (2) INFORMATION FOR SEQ ID NO: 17: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe Gln Cys Arg Ile Cys Met Arg Asn Phe

(2) INFORMATION FOR SEQ ID NO: 15:

5 10

Ser Gln Ala Gln Asp Leu Gln Arg His Leu
15 20

Lys His Thr Gly Glu Lys
25

	(2)	INFORMATION	FOR	SEO	ID	NO:	18:
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1	′ i '	) CEOHENCE	CHARACTERISTICS:	
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- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Glu Glu Lys Pro Phe Gln Cys Arg
5

Ser Leu Thr Arg His Thr Arg Thr His Thr 25 30

Gly Glu Lys Pro Phe Gln Cys Arg Ile Cys 35 40

Met Arg Asn Phe Ser Asp Arg Ser His Leu 45 50

Thr Arg His Thr Arg Thr His Thr Gly Glu
55 60

Lys Pro Phe Gln Cys Arg Ile Cys Met Arg 65 70

Asn Phe Ser Asp Arg Ser Asn Leu Thr Arg
75 80

His Thr Arg Thr His Thr Gly Glu Lys 85